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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/883,797

DATE: 11/27/2001  
 TIME: 12:54:48

Input Set : N:\Crf3\RULE60\09883797.raw  
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1 <110> APPLICANT: Jaworski, Jan G.  
 2 Post-Beittenmiller, Martha A.  
 3 Todd, James  
 4 <120> TITLE OF INVENTION: FATTY ACID ELONGASES  
 5 <130> FILE REFERENCE: 07148/064001  
 6 <140> CURRENT APPLICATION NUMBER: 09/883,797  
 7 <141> CURRENT FILING DATE: 2001-06-18  
 8 <150> PRIOR APPLICATION NUMBER: 08/868,373  
 9 <151> PRIOR FILING DATE: 1997-06-03  
 10 <160> NUMBER OF SEQ ID NOS: 22  
 11 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
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 16 <213> ORGANISM: Arabidopsis thaliana  
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 20 ggacttcaca actcttgcaa cgtgaccacc attctcttct tcttaattat tcttccttta 180  
 21 accggaaccg tgctggttca gctaaccggg ctaacgttgc atacgttctc tgagcttgg 240  
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 23 ttcgttttga ccctctacgt ggctaaaccgg tctaaaccgg ttaccttagt ggatttctcc 360  
 24 tgctacaaac cggaaagacga gctgtaaaata tcagtagatt cgttcttgac gatgactgag 420  
 25 gaaaatggat cattcaccga tgacacgggt cagttccagc aaagaatctc gaaccgggccc 480  
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 28 gagaaaaaccg gaattaaacc ggccgaagtc ggaatcttga tagtaaactg cagcttattc 660  
 29 aatccgcacgc cgtctctatc agcgtatgtc gtgaaccatt acaagatgag agaagacatc 720  
 30 aaaagttaca acctcggagg aatgggttgc tccggccggat taatctcaat cgatctcgct 780  
 31 aacaatctcc tcaaagcaaa ccctaattct tacgctgtcg tggtaagcac ggaaaacata 840  
 32 accctaaact ggtacttcgg aaatgaccgg tcaatgtcc tctgcaactg catcttccga 900  
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 38 aaaccgtata ttccggattt caagcttagt ttgcggcatt tctgtattca cgcaggaggt 1260  
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 45 <210> SEQ ID NO: 2  
 46 <211> LENGTH: 520  
 47 <212> TYPE: PRT  
 48 <213> ORGANISM: Arabidopsis thaliana  
 49 <400> SEQUENCE: 2

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 52 Ser Ala Val Ile Arg Ile Arg Arg Arg Leu Pro Asp Leu Leu Thr Ser  
 53 20 25 30  
 54 Val Lys Leu Lys Tyr Val Lys Leu Gly Leu His Asn Ser Cys Asn Val  
 55 35 40 45  
 56 Thr Thr Ile Leu Phe Phe Leu Ile Ile Leu Pro Leu Thr Gly Thr Val  
 57 50 55 60  
 58 Leu Val Gln Leu Thr Gly Leu Thr Phe Asp Thr Phe Ser Glu Leu Trp  
 59 65 70 75 80  
 60 Ser Asn Gln Ala Val Gln Leu Asp Thr Ala Thr Arg Leu Thr Cys Leu  
 61 85 90 95  
 62 Val Phe Leu Ser Phe Val Leu Thr Leu Tyr Val Ala Asn Arg Ser Lys  
 63 100 105 110  
 64 Pro Val Tyr Leu Val Asp Phe Ser Cys Tyr Lys Pro Glu Asp Glu Arg  
 65 115 120 125  
 66 Lys Ile Ser Val Asp Ser Phe Leu Thr Met Thr Glu Glu Asn Gly Ser  
 67 130 135 140  
 68 Phe Thr Asp Asp Thr Val Gln Phe Gln Gln Arg Ile Ser Asn Arg Ala  
 69 145 150 155 160  
 70 Gly Leu Gly Asp Glu Thr Tyr Leu Pro Arg Gly Ile Thr Ser Thr Pro  
 71 165 170 175  
 72 Pro Lys Leu Asn Met Ser Glu Ala Arg Ala Glu Ala Glu Ala Val Met  
 73 180 185 190  
 74 Phe Gly Ala Leu Asp Ser Leu Phe Glu Lys Thr Gly Ile Lys Pro Ala  
 75 195 200 205  
 76 Glu Val Gly Ile Leu Ile Val Asn Cys Ser Leu Phe Asn Pro Thr Pro  
 77 210 215 220  
 78 Ser Leu Ser Ala Met Ile Val Asn His Tyr Lys Met Arg Glu Asp Ile  
 79 225 230 235 240  
 80 Lys Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser  
 81 245 250 255  
 82 Ile Asp Leu Ala Asn Asn Leu Leu Lys Ala Asn Pro Asn Ser Tyr Ala  
 83 260 265 270  
 84 Val Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Phe Gly Asn  
 85 275 280 285  
 86 Asp Arg Ser Met Leu Leu Cys Asn Cys Ile Phe Arg Met Gly Gly Ala  
 87 290 295 300  
 88 Ala Ile Leu Leu Ser Asn Arg Arg Gln Asp Arg Lys Lys Ser Lys Tyr  
 89 305 310 315 320  
 90 Ser Leu Val Asn Val Val Arg Thr His Lys Gly Ser Asp Asp Lys Asn  
 91 325 330 335  
 92 Tyr Asn Cys Val Tyr Gln Lys Glu Asp Glu Arg Gly Thr Ile Gly Val  
 93 340 345 350  
 94 Ser Leu Ala Arg Glu Leu Met Ser Val Ala Gly Asp Ala Leu Lys Thr  
 95 355 360 365  
 96 Asn Ile Thr Thr Leu Gly Pro Met Val Leu Pro Leu Ser Glu Gln Leu  
 97 370 375 380  
 98 Met Phe Leu Ile Ser Leu Val Lys Arg Lys Met Phe Lys Leu Lys Val

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102	His Ala Gly Gly Arg Ala Val Leu Asp Glu Val Gln Lys Asn Leu Asp			
103	420	425	430	
104	Leu Lys Asp Trp His Met Glu Pro Ser Arg Met Thr Leu His Arg Phe			
105	435	440	445	
106	Gly Asn Thr Ser Ser Ser Leu Trp Tyr Glu Met Ala Tyr Thr Glu			
107	450	455	460	
108	Ala Lys Gly Arg Val Lys Ala Gly Asp Arg Leu Trp Gln Ile Ala Phe			
109	465	470	475	480
110	Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Pro			
111	485	490	495	
112	Val Ser Thr Glu Glu Met Thr Gly Asn Ala Trp Ala Gly Ser Ile Asp			
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124	caagatctcc aaaacttta cctctactta caaaaacaacc acacatctct aaccatgttc	180		
125	ttcccttacc tcgctctcggt gtcgactctt tacctcatga cccggcccaa acccgtttat	240		
126	ctcggtactt ttagctgcta cctcccaccc tcgcacatctca aagccagcac ccagaggatc	300		
127	atgcaacacg taaggcttgc acgagaagca ggcgcgtgga agcaagagtc cgattacttg	360		
128	atggacttct gcgagaagat tctagaacgt tccggctctag gccaagagac gtacgtaccc	420		
129	gaaggtcttc aaactttgcc actacaacag aattttggctg tatcacgtat agagacggag	480		
130	gaagttatta ttgggtcggt cgataatctg tttcgcaca cgggataaag cccttagtgat	540		
131	ataggtatat ttgggtgtgaa ttcaagcact tttaatccaa cacccgcgt atcaagtatc	600		
132	ttagtgaata agttttaact tagggataat ataaagagct tgaatcttgg tgggatgggg	660		
133	tgtagcgctg gagtcatcgca tacatcgatgcg gctaagagct ttgttacaagt tcataaaaaac	720		
134	actttatgctc ttgtggtagt cacggagaac atcactcaaa acttgcacat gggtaacaac	780		
135	aaatcaatgt ttggttacaaa ctgtttgttc cgtataggtg gggccgcgtat ttgcgtttct	840		
136	aaccggctca tagatcgtaa acgcgcacaa tacgagcttgc ttccacaccgt gcgggtccat	900		
137	accggagcag atgaccgatc ctatgaatgt gcaactcaag aagaggatga agatggcata	960		
138	gttgggggtt ccttgtcaaa gaatctacca atggtagctg caagaaccct aaagatcaat	1020		
139	atcgcaactt ttgggtccgct ttttcttccc ataagcgaga agtttcactt ctttgcgagg	1080		
140	ttcggtaaaa agaagttct caaccccaag ctaaagcatt acattccgga tttcaagctc	1140		
141	gcattcgagc atttctgtat ccatgcgggtt ggttagagcgc taatttgatga gatggagaag	1200		
142	aatcttcatc taactccact agacgttgcg gcttcaagaa tgacattaca caggtttgg	1260		
143	aataccctttt ctagctccat ttggtagcggat ttgggttaca cagaagccaa aggaaggatg	1320		
144	acgaaaggag ataggatttg gcagattgcg ttggggtcg gttttaagtg taatagttca	1380		
145	gttgggggtt ctcttcgtaa cgtcaagccct tctactaata atccttggga acagtgtcta	1440		
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151 <213> ORGANISM: Arabidopsis thaliana  
152 <400> SEQUENCE: 4  
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156 20 25 30  
157 Val Glu Ala Ser Arg Leu Ser Thr Gln Asp Leu Gln Asn Phe Tyr Leu  
158 35 40 45  
159 Tyr Leu Gln Asn Asn His Thr Ser Leu Thr Met Phe Phe Leu Tyr Leu  
160 50 55 60  
161 Ala Leu Gly Ser Thr Leu Tyr Leu Met Thr Arg Pro Lys Pro Val Tyr  
162 65 70 75 80  
163 Leu Val Asp Phe Ser Cys Tyr Leu Pro Pro Ser His Leu Lys Ala Ser  
164 85 90 95  
165 Thr Gln Arg Ile Met Gln His Val Arg Leu Val Arg Glu Ala Gly Ala  
166 100 105 110  
167 Trp Lys Gln Glu Ser Asp Tyr Leu Met Asp Phe Cys Glu Lys Ile Leu  
168 115 120 125  
169 Glu Arg Ser Gly Leu Gly Gln Glu Thr Tyr Val Pro Glu Gly Leu Gln  
170 130 135 140  
171 Thr Leu Pro Leu Gln Gln Asn Leu Ala Val Ser Arg Ile Glu Thr Glu  
172 145 150 155 160  
173 Glu Val Ile Ile Gly Ala Val Asp Asn Leu Phe Arg Asn Thr Gly Ile  
174 165 170 175  
175 Ser Pro Ser Asp Ile Gly Ile Leu Val Val Asn Ser Ser Thr Phe Asn  
176 180 185 190  
177 Pro Thr Pro Ser Leu Ser Ser Ile Leu Val Asn Lys Phe Lys Leu Arg  
178 195 200 205  
179 Asp Asn Ile Lys Ser Leu Asn Leu Gly Gly Met Gly Cys Ser Ala Gly  
180 210 215 220  
181 Val Ile Ala Ile Asp Ala Ala Lys Ser Leu Leu Gln Val His Arg Asn  
182 225 230 235 240  
183 Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Leu Tyr  
184 245 250 255  
185 Met Gly Asn Asn Lys Ser Met Leu Val Thr Asn Cys Leu Phe Arg Ile  
186 260 265 270  
187 Gly Gly Ala Ala Ile Leu Leu Ser Asn Arg Ser Ile Asp Arg Lys Arg  
188 275 280 285  
189 Ala Lys Tyr Glu Leu Val His Thr Val Arg Val His Thr Gly Ala Asp  
190 290 295 300  
191 Asp Arg Ser Tyr Glu Cys Ala Thr Gln Glu Glu Asp Glu Asp Gly Ile  
192 305 310 315 320  
193 Val Gly Val Ser Leu Ser Lys Asn Leu Pro Met Val Ala Ala Arg Thr  
194 325 330 335  
195 Leu Lys Ile Asn Ile Ala Thr Leu Gly Pro Leu Val Leu Pro Ile Ser  
196 340 345 350  
197 Glu Lys Phe His Phe Phe Val Arg Phe Val Lys Lys Lys Phe Leu Asn  
198 355 360 365

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 201 Phe Cys Ile His Ala Gly Gly Arg Ala Leu Ile Asp Glu Met Glu Lys  
 202 385 390 395 400  
 203 Asn Leu His Leu Thr Pro Leu Asp Val Glu Ala Ser Arg Met Thr Leu  
 204 405 410 415  
 205 His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu Leu Ala  
 206 420 425 430  
 207 Tyr Thr Glu Ala Lys Gly Arg Met Thr Lys Gly Asp Arg Ile Trp Gln  
 208 435 440 445  
 209 Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala  
 210 450 455 460  
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 223 gcaggattag ccatgaaagg atctaagatc aacgtagaag atctccaaaa gttctccctc 180  
 224 caccatacac agaacaacct ccaaaccata agcctctat tgtttctgt cgttttgtg 240  
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 242 ccgttacacg tagagggcgtc aagaatgaca ctacacaggt ttggtaacac ttcttctagc 1320  
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 248 <210> SEQ ID NO: 6  
 249 <211> LENGTH: 504

VERIFICATION SUMMARY

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